



Expression variation in connected recombinant populations of *Arabidopsis thaliana* highlights distinct transcriptome architectures

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Titre	Expression variation in connected recombinant populations of <i>Arabidopsis thaliana</i> highlights distinct transcriptome architectures
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Auteur	Cubillos, Francisco A [1], Yansouni, Jennifer [2], Khalili, Hamid [3], Balzergue, Sandrine [4], Elftieh, Samira [5], Martin-Magniette, Marie-Laure [6], Serrand, Yann [7], Lepiniec, Loïc [8], Baud, Sébastien [9], Dubreucq, Bertrand [10], Renou, Jean-Pierre [11], Camilleri, Christine [12], Loudet, Olivier [13]
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Résumé en anglais	Expression traits can vary quantitatively between individuals and have a complex inheritance. Identification of the genetics underlying transcript variation can help in the understanding of phenotypic variation due to genetic factors regulating transcript abundance and shed light into divergence patterns. So far, only a limited number of studies have addressed this subject in <i>Arabidopsis</i> , with contrasting results due to dissimilar statistical power. Here, we present the transcriptome architecture in leaf tissue of two RIL sets obtained from a connected-cross design involving 3 commonly used accessions. We also present the transcriptome architecture observed in developing seeds of a third independent cross.
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